This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (ORIGINAL) A method for the detection of a target nucleic acid molecule, comprising:

a) exposing the target nucleic acid molecule to a first complementation molecule and a second complementation molecule, wherein the first complementation molecule comprises a first polypeptide portion coupled to a first probe portion, wherein the first probe portion binds to a first nucleic acid hybridization site, and wherein the second complementation molecule comprises a second polypeptide portion coupled to a second probe portion, wherein the second probe portion binds to a second nucleic acid hybridization site, and wherein the first and second nucleic acid sites are selected to that when the sites are in close proximity to each other then the first and second polypeptide portions of the first and second complementation molecules interact and form an assembled complementation complex;

b) allowing the components to react under conditions that permit the formation of an assembled complementation complex; and

c) determining if an assembled complementation complex is present by any means which allows detection of the assembled complex but not the individual polypeptide portions.

2. (ORIGINAL) The method of claim 1, wherein the first and second polypeptides interact in the complementation complex to form an active enzyme.

3. (ORIGINAL) The method of claim 1, wherein the first and second polypeptides interact in the complementation complex to form an assembled protein with detectable fluorogenic activity.

4. (ORIGINAL) The method of claim 1, wherein the first and second polypeptides interact in the complementation complex to form an assembled protein which contains a discontinuous epitope, which may be detected by use of an antibody which specifically recognizes the discontinuous epitope on the assembled protein but not the partial epitope present on either individual polypeptide.

5. (ORIGINAL) The method of claim 1, wherein the target nucleic acid is detected *in vivo* or *in vitro*.

6. (ORIGINAL) The method of claim 5, wherein the target nucleic acid is detected *in vivo*.

7. (ORIGINAL) The method of claim 1, wherein the target nucleic acid is single-stranded or double-stranded.

8. (ORIGINAL) The method of claim 2, wherein the active enzyme is detected by a chromogenic or fluorogenic reaction.

9. (ORIGINAL) The method of claim 8, wherein the enzyme is dihydrofolate reductase or β-lactamase.

10. (ORIGINAL) The method of claim 3, wherein the assembled protein is a fluorescent protein.

11. (ORIGINAL) The method of claim 10, wherein the fluorescent protein is a natural, modified, or genetically engineered fluorescent protein.

12. (ORIGINAL) The method of claim 11, wherein the fluorescent protein is selected from the group consisting of GFP, EGFP, CFP, YFP, and RFP.

13. (ORIGINAL) The method of claim 1, wherein the first probe portion and the second probe portion are selected from the group consisting of nucleic acids, nucleic acid analogues, and nucleic-acid binding polypeptides.

14. (ORIGINAL) The method of claim 13, wherein the first probe portion and the second probe portion are oligonucleotides.

15. (ORIGINAL) The method of claim 13, wherein the first probe portion and the second probe portion are nucleic-acid binding polypeptides which interact with the target nucleic acid with high affinity.

16. (ORIGINAL) The method of claim 1, wherein the probe portion and the polypeptide portion of each complementation molecule is coupled by a flexible linker.

17. (ORIGINAL) The method of claim 1, wherein the target nucleic acid is amplified prior to exposure to the first and second complementation molecules.

18. (ORIGINAL) The method of claim 17, wherein the target nucleic acid is amplified using rolling circle amplification to generate a single-stranded DNA target with a multiplicity of the same hybridization sites.

19. (ORIGINAL) The method of claim 1, wherein the first and the second probes bind to two adjacent sequences in the target nucleic acid.

20. (ORIGINAL) The method of claim 1, wherein the first and the second probes bind to the same sequence in the target nucleic acid.

21. (ORIGINAL) A kit for the detection of a target nucleic acid molecule, wherein the kit comprises a vial containing a first complementation molecule and a vial containing a second complementation molecule, wherein the first complementation molecule comprises a first polypeptide portion coupled to a first probe portion, wherein the first probe portion binds to a first nucleic acid hybridization site, and wherein the second complementation molecule comprises a second polypeptide portion coupled to a second probe portion, wherein the second probe portion binds to a second nucleic acid hybridization site, and wherein the first and second nucleic acid sites are selected such that when the sites are in close proximity to each other then the

first and second polypeptide portions of the first and second complementation molecules interact and form an assembled complementation complex when the target nucleic acid molecule is exposed to the first and second complementation molecules.

22. (ORIGINAL) The kit of claim 21, wherein the first and second polypeptides interact in the complementation complex to form an active enzyme.

23. (ORIGINAL) The kit of claim 21, wherein the first and second polypeptides interact in the complementation complex to form an assembled protein with detectable fluorogenic activity.

24. (ORIGINAL) The kit of claim 21, wherein the first and second polypeptides interact in the complementation complex to form an assembled protein which contains a discontinuous epitope, which may be detected by use of an antibody which specifically recognizes the discontinuous epitope on the assembled protein but not the partial epitope present on either individual polypeptide.